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L12: Entry 1 of 1 File: DWPI Sep 13, 2000

DERWENT-ACC-NO: 1999-347467
DERWENT-WEEK: 200046

TITLE: Nucleic acid flanked by binding sites for SB transposase - used to identify enhancers and coding sequences and for gene transfer

INVENTOR: CLARK, K J; DUPUY, A J ; EKKER, S C ; HACKETT, P B ; IVICS, Z ; IZSVAK, Z ; LARGAESPADA, D A

PATENT-ASSIGNEE:

ASSIGNEE	CODE
UNIV MINNESOTA	MINU

PRIORITY-DATA:
1997US-0065303 November 13, 1997

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
EP 1034258 A2	September 13, 2000	E	000	C12N015/00
WO 9925817 A2	May 27, 1999	E	136	C12N015/00
AU 9914103 A	June 7, 1999	N/A	000	C12N015/00

DESIGNATED-STATES: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZW AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

APPLICATION-DATA:

PUB-NO	APPL-DESCRIPTOR	APPL-NO	APPL-NO
EP 1034258A2	November 13, 1998	1998EP-0957974	N/A
EP 1034258A2	November 13, 1998	1998WO-US24348	N/A
EP 1034258A2	N/A	WO 9925817	Based on
WO 9925817A2	November 13, 1998	1998WO-US24348	N/A
AU 9914103A	November 13, 1998	1999AU-0014103	N/A
AU 9914103A	N/A	WO 9925817	Based on

INT-CL (IPC): C12N 15/00

RELATED-ACC-NO: 1998-531525

ABSTRACTED-PUB-NO: WO 9925817A
BASIC-ABSTRACT:

NOVELTY - Nucleic acid fragment (A) comprises a coding sequence (I) positioned between at least 2 inverted repeats (IR) that can bind to an SB protein (transposase). DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (a) method for identifying an enhancer in a cell by inserting: (i) (A) in which (I) encodes a marker and is under control of a weak promoter, and (ii) a transposase source, then detecting the marker in the cell (or its progeny) to indicate that (A) has integrated into a DNA domain that contains an enhancer; (b) method for identifying a genomic coding sequence by a method similar to (a) but where (A) also contains a splice acceptor site (SAS) and internal ribosome entry site (IRES), both linked to the marker-encoding sequence; (c) method for identifying the function of an analyte coding sequence by a method similar to (a) but where (A) also includes the analyte sequence (5'-to the marker) and an IRES, and detection of any change in phenotype of marker-expressing cells; (d) gene transfer system comprising (A) and either an SB protein or nucleic acid encoding it; (e) preparation of a transgenic animal by introducing (A), containing a heterologous sequence, into a cell, also animals and their progeny produced this way; (f) gene transfer system for introducing (I) into the DNA of a fish comprising (I) that includes an IRES and is able to integrate into the genome; and (h) transgenic fish, or their cells, containing a heterologous IRES.

USE - (A) are used: (i) to identify expression control sequences (particularly enhancers) and coding sequences (or their functions); (ii) to deliver nucleic acid to the DNA of a cell, for production of transgenic animals, including fish, e.g. for use in production of therapeutic proteins or to impart desirable traits such as increased growth or disease resistance, and (iii) for gene therapy of e.g. immune system disorders, cancer, phenylketonuria.

ACTIVITY - None given.

MECHANISM OF ACTION - SB transposase catalyzes insertion of DNA into cellular DNA.

SB catalyzes integration of (I) into a wide variety of cell types and in many different species, eliminating the need for viral gene-transfer systems. It can deliver fragments of 1.3-5 kb.

CHOSEN-DRAWING: Dwg.0/16

TITLE-TERMS: NUCLEIC ACID FLANK BIND SITE IDENTIFY ENHANCE CODE SEQUENCE GENE TRANSFER

DERWENT-CLASS: B04 C06 D16

CPI-CODES: B02-N; C02-N; B04-E02; C04-E02; B04-F0100E; C04-F0100E; B04-F0200E; C04-F0200E; B04-L05A; C04-L05A; B04-N02; C04-N02; B04-P0100E; C04-P0100E; B11-C08E1; C11-C08E1; B12-K04F; C12-K04F; B14-G02D; C14-G02D; B14-H01; C14-H01; B14-S03; C14-S03; D05-H09; D05-H11; D05-H12A; D05-H12E; D05-H14B2; D05-H16A; D05-H17A3;

CHEMICAL-CODES:

Chemical Indexing M1 *01*

Fragmentation Code
M423 M430 M710 M782 M903 N102 N135 P433 P633 P831
Q233 V753

Chemical Indexing M1 *02*
Fragmentation Code
M423 M430 M782 M903 N102 P831 Q233 V802 V812 V813

Chemical Indexing M1 *03*
Fragmentation Code
M423 M430 M760 M782 M903 N102 N135 P831 Q233 V754

Chemical Indexing M1 *04*
Fragmentation Code
M423 M750 M903 N102 Q233 V752

Chemical Indexing M1 *05*
Fragmentation Code
M423 M710 M720 M903 N134 N135 N136 Q233 V600 V644
V754

Chemical Indexing M2 *06*
Fragmentation Code
F012 F013 F014 F015 F016 F123 G037 G563 H1 H101
H121 H162 H181 H4 H404 H422 H462 H5 H521 H8
K0 L8 L814 L821 L834 M1 M126 M141 M280 M311
M321 M342 M373 M391 M413 M510 M521 M530 M541 M750
M903 M904 N102 Q233 V0 V141
Specfic Compounds
03870A 03870K

Chemical Indexing M2 *07*
Fragmentation Code
F012 F013 F014 F015 F016 F019 F113 F123 F199 G037
G563 H1 H100 H122 H162 H182 H4 H405 H424 H461
H481 H5 H523 H8 K0 L8 L812 L814 L818 L819
L821 L822 L831 L834 M1 M126 M129 M141 M149 M280
M311 M323 M342 M373 M393 M413 M510 M523 M530 M541
M750 M800 M903 M904 N102 Q233 V0 V141
Specfic Compounds
03869A 03869K

Chemical Indexing M2 *08*
Fragmentation Code
F012 F013 F014 F015 F016 F019 F113 F123 F199 G037
G563 H1 H101 H122 H162 H182 H4 H405 H424 H461
H481 H5 H523 H8 K0 L8 L812 L814 L822 L834
M1 M126 M129 M141 M149 M280 M311 M323 M342 M373
M393 M413 M510 M523 M530 M541 M750 M800 M903 M904
N102 Q233
Specfic Compounds
18274A 18274K

Chemical Indexing M2 *09*
Fragmentation Code
F012 F013 F014 F015 F016 F019 F113 F123 F199 G037
G563 H1 H101 H122 H162 H181 H4 H405 H424 H461
H482 H5 H523 H8 K0 L8 L812 L814 L818 L821
L822 L831 L834 M1 M126 M129 M141 M149 M280 M311
M323 M342 M373 M393 M413 M510 M523 M530 M541 M750
M903 M904 M910 N102 Q233 V0 V160
Specfic Compounds
01684A 01684K
Registry Numbers
1684U

Chemical Indexing M6 *10*
Fragmentation Code
M903 P831 Q233 R515 R521 R614 R624 R627 R633 R637

UNLINKED-DERWENT-REGISTRY-NUMBERS: 1684U

SECONDARY-ACC-NO:
CPI Secondary Accession Numbers: C1999-102253